

**S3 Table. Ribosome profiling reads processing and alignment statistics.**

Sample	SRR Run	Total reads processed	Reads $\geq$ 15 bp & contained adapters	Reads not aligned to ncRNAs*	Duplicate reads	Reads aligned to transcriptome
<i>SUP45</i> , 25°C (replicate 1)	SRR13208091	67,532,129	57,853,137	25,787,398	3,441,725	20,407,888
<i>SUP45</i> , 25°C (replicate 2)	SRR13208092	61,556,833	51,451,140	18,867,321	7,016,422	10,101,506
<i>SUP45</i> , 37°C (replicate 1)	SRR13208093	49,805,337	44,462,117	14,274,514	1,866,021	11,195,529
<i>SUP45</i> , 37°C (replicate 2)	SRR13208094	64,613,280	55,971,740	24,346,626	5,660,607	16,685,974
<i>sup45-ts</i> , 25°C (replicate 1)	SRR13208095	91,931,471	70,972,671	34,574,953	5,747,485	24,437,810
<i>sup45-ts</i> , 25°C (replicate 2)	SRR13208096	60,891,476	49,432,024	25,181,918	4,148,599	18,939,808
<i>sup45-ts</i> , 37°C (replicate 1)	SRR13208097	77,154,540	55,550,470	21,351,921	3,510,551	14,378,321
<i>sup45-ts</i> , 37°C (replicate 2)	SRR13208098	66,416,665	48,944,777	17,330,578	3,701,109	10,930,634
<i>SUP45-D</i> (replicate 1)	SRR7241903	54,157,010	53,979,859	39,261,094	N/A	39,261,094
<i>SUP45-D</i> (replicate 2)	SRR7241904	32,548,315	32,188,657	21,139,968	N/A	21,139,968
<i>sup45-d</i> (replicate 1)	SRR7241908	46,687,648	45,226,887	34,527,078	N/A	34,527,078
<i>sup45-d</i> (replicate 2)	SRR7241909	32,916,353	32,750,862	20,325,474	N/A	20,325,474
<i>RLI1-D</i> (replicate 1)	SRR2046309	52,021,032	51,768,936	17,545,223	N/A	17,545,223
<i>RLI1-D</i> (replicate 2)	SRR2046310	52,026,256	49,283,307	41,880,568	N/A	41,880,568
<i>rli1-d</i> (replicate 1)	SRR2046311	46,386,847	45,694,917	15,064,692	N/A	15,064,692
<i>rli1-d</i> (replicate 2)	SRR2046312	158,583,030	155,589,606	53,259,434	N/A	53,259,434
<i>rli1-d</i> (replicate 3)	SRR2046319	35,129,965	33,633,653	28,658,467	N/A	28,658,467

\*ncRNAs refer to non protein-coding RNAs